GenCore version 5.1.4_p5_4578

OM nucleic - nucleic search, using sw model

Run on: March 11, 2003, 07:22:43 ; Search time 152 Seconds
(without alignments)
14650.296 Million cell updates/sec

Title: US-10-046-433-39
Perfect score: 3334
Sequence: 1 gcagaagcagcagccgcagc.....attaaaaaaaaaaaaaaaaa 3334

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 478924 seqs, 333959956 residues

Total number of hits satisfying chosen parameters: 957848

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	3303.4	99.1	3501	9	US-10-028-072-37	Sequence 37, Appl
	2	3303.4	99.1	3501	9	US-10-121-049-37	Sequence 37, Appl
	3	3303.4	99.1	3501	9	US-10-123-904-37	Sequence 37, Appl
	4	3303.4	99.1	3501	9	US-10-140-470-37	Sequence 37, Appl
	5	3303.4	99.1	3501	9	US-10-175-746-37	Sequence 37, Appl
	6	3303.4	99.1	3501	9	US-10-176-918-37	Sequence 37, Appl
	7	3303.4	99.1	3501	9	US-10-176-921-37	Sequence 37, Appl
	8	3303.4	99.1	3501	9	US-10-137-865-37	Sequence 37, Appl
	9	3303.4	99.1	3501	9	US-10-140-474-37	Sequence 37, Appl
	10	3303.4	99.1	3501	9	US-10-142-431-37	Sequence 37, Appl
	11	3303.4	99.1	3501	9	US-10-143-114-37	Sequence 37, Appl
	12	3303.4	99.1	3501	9	US-10-140-002-37	Sequence 37, Appl
	13	551	16.5	625	9	US-09-925-299-209	Sequence 209, App
	14	551	16.5	625	10	US-09-925-299-209	Sequence 209, App
	15	537.6	16.1	1737	9	US-10-002-050-19	Sequence 19, Appl
	16	537.6	16.1	1737	9	US-10-002-304-19	Sequence 19, Appl
	17	537.6	16.1	1737	12	US-10-003-152-19	Sequence 19, Appl
c	18	424.4	12.7	426	9	US-09-736-457-913	Sequence 913, App
c	19	424.4	12.7	426	9	US-09-902-941-913	Sequence 913, App
c	20	424.4	12.7	426	9	US-09-849-626-913	Sequence 913, App
	21	419.8	12.6	1508	9	US-10-002-050-9	Sequence 9, Appli
	22	419.8	12.6	1508	9	US-10-002-304-9	Sequence 9, Appli
	23	419.8	12.6	1508	12	US-10-003-152-9	Sequence 9, Appli
	24	364	10.9	400	10	US-09-998-598-2567	Sequence 2567, Ap
c	25	284.4	8.5	466	10	US-09-815-343-754	Sequence 754, App
c	26	282.4	8.5	306	10	US-09-969-708-595	Sequence 595, App
	27	263.4	7.9	265	9	US-09-736-457-864	Sequence 864, App
	28	263.4	7.9	265	9	US-09-902-941-864	Sequence 864, App
	29	263.4	7.9	265	9	US-09-849-626-864	Sequence 864, App
c	30	189.6	5.7	231	9	US-10-076-622-45	Sequence 45, Appl
c	31	189.6	5.7	231	10	US-09-604-287A-45	Sequence 45, Appl
c	32	189.6	5.7	231	10	US-09-339-338-45	Sequence 45, Appl
c	33	189.6	5.7	231	12	US-10-007-805-45	Sequence 45, Appl
	34	130.8	3.9	160	9	US-10-076-622-44	Sequence 44, Appl
	35	130.8	3.9	160	10	US-09-604-287A-44	Sequence 44, Appl
	36	130.8	3.9	160	10	US-09-339-338-44	Sequence 44, Appl
	37	130.8	3.9	160	12	US-10-007-805-44	Sequence 44, Appl
	38	118.8	3.6	333	10	US-09-783-590-3589	Sequence 3589, Ap
	39	110.8	3.3	432	10	US-09-960-352-5091	Sequence 5091, Ap
	40	98.6	3.0	192	9	US-10-092-750-108	Sequence 108, App
	41	92.8	2.8	96	9	US-10-092-750-189	Sequence 189, App
c	42	89	2.7	244	10	US-09-864-761-22945	Sequence 22945, A
c	43	76.6	2.3	371	10	US-09-864-761-6225	Sequence 6225, Ap
c	44	71.4	2.1	196	10	US-09-864-761-30975	Sequence 30975, A
c	45	71.4	2.1	457	10	US-09-864-761-14419	Sequence 14419, A

ALIGNMENTS

RESULT 1
US-10-028-072-37
; Sequence 37, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
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; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

Query Match 99.1%; Score 3303.4; DB 9; Length 3501;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3321; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

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Qy    181 ACGGGACCGGAGCTTCACGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 240
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Qy    241 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGGCCTGTGCACCAGC 300
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Qy    421 ATTCGGTTTGATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 480
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Db    796 AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 855

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Db   1096 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1155

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Db   1156 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1215

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Qy   1741 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1816 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1875

Qy   1801 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1876 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1935

Qy   1861 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1936 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1995
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Qy   1921 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1996 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 2055

Qy   1981 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2056 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2115

Qy   2041 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2116 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2175

Qy   2101 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2176 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2235

Qy   2161 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2236 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2295

Qy   2221 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2296 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2355

Qy   2281 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2356 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2415

Qy   2341 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2416 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2475

Qy   2401 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2476 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2535

Qy   2461 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2536 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2595

Qy   2521 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2596 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2655

Qy   2581 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2656 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2715

Qy   2641 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGAAGACTACTTACGTG 2700
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db   2716 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGANGACTACTTACGTG 2775

Qy   2701 TGGCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2760
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2776 TGNCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2835

Qy   2761 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2836 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2895

Qy   2821 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2896 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2955

Qy   2881 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2956 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 3015

Qy   2941 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAA-TCACTC 2999
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||| |||||
Db   3016 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAAGTCACTT 3075

Qy   3000 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3059
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3076 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3135

Qy   3060 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3119
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3136 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3195

Qy   3120 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3179
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3196 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3255

Qy   3180 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3256 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3315

Qy   3240 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3299
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3316 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3375

Qy   3300 ACACTTTGTTTGTAAATTAAAAAAAAAAAAAAAAA 3334
          ||| ||| ||| ||| ||||||||||||||||||
Db   3376 ACATTTTTTTTTAAAAAAAAAAAAAAAAAAAAAA 3410
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RESULT 2
US-10-121-049-37
; Sequence 37, Application US/10121049
; Publication No. US20030022239A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C17
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2002-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 37
; LENGTH: 3501
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2762, 2778
; OTHER INFORMATION: unknown base
US-10-121-049-37

Query Match 99.1%; Score 3303.4; DB 9; Length 3501;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3321; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

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Qy      1 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     76 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 135

Qy     61 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGGGAAGAACTGAGAGGCGC 120
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            ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db      136 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGAGAAGAACTGAGAGGCGC 195

Qy      121 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      196 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 255

Qy      181 ACGGGACCGGAGCTTCACGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 240
            ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db      256 ACGGGACCGGAGCTTCATGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 315

Qy      241 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGGCCTGTGCACCAGC 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      316 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGGCCTGTGCACCAGC 375

Qy      301 CTGCCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCCGGGGAGTTTCTG 360
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      376 CTGTCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCCGGGGAGTTTCTG 435

Qy      361 GATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      436 GATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 495

Qy      421 ATTCGGTTTGATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      496 ATTCGGTTTGATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 555

Qy      481 GAGCTGGATGACAGTGCTGCTGAGTCCACCGGGAACTGTACTTCGTCCAAGTGGGTTCCC 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      556 GAGCTGGATGACAGTGCTGCTGAGTCCACCGGGAACTGTACTTCGTCCAAGTGGGTTCCC 615

Qy      541 CGGGGCGACTACATCGCCTTCAACACGGACGAATGCACAGCCACACTGATGTACGCCGTC 600
            ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db      616 CGGGGCGACTACATCGCCTCCAACACGGACGAATGCACAGCCACACTGATGTACGCCGTC 675

Qy      601 AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATCATC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      676 AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATCATC 735

Qy      661 TTTGAGTTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGGATG 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      736 TTTGAGTTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGGATG 795

Qy      721 AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      796 AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 855

Qy      781 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      856 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 915

Qy      841 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      916 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 975

Qy      901 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCA 960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      976 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCA 1035

Qy      961 AATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1020
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1036 AATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1095

Qy     1021 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1096 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1155

Qy     1081 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1156 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1215

Qy     1141 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1216 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1275

Qy     1201 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1276 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1335

Qy     1261 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1336 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1395

Qy     1321 GAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1396 GAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 1455

Qy     1381 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1456 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1515

Qy     1441 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTTAGACCT 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1516 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTTAGACCT 1575

Qy     1501 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1576 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1635

Qy     1561 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1636 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1695

Qy     1621 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1696 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1755

Qy     1681 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1740
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1756 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1815

Qy     1741 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1816 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1875

Qy     1801 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1876 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1935

Qy     1861 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1936 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1995

Qy     1921 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1996 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 2055

Qy     1981 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2056 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2115

Qy     2041 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2116 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2175

Qy     2101 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2176 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2235

Qy     2161 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2236 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2295

Qy     2221 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2296 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2355
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Qy    2281 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2356 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2415

Qy    2341 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2416 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2475

Qy    2401 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2476 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2535

Qy    2461 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2536 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2595

Qy    2521 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2596 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2655

Qy    2581 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2656 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2715

Qy    2641 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGAAGACTACTTACGTG 2700
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2716 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGAAGACTACTTACGTG 2775

Qy    2701 TGGCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2760
           || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2776 TGNCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2835

Qy    2761 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2836 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2895

Qy    2821 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2896 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2955

Qy    2881 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2956 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 3015

Qy    2941 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAA-TCACTC 2999
           |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db    3016 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAAGTCACTT 3075

Qy    3000 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3059
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3076 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3135

Qy    3060 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3119
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3136 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3195

Qy    3120 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3179
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3196 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3255

Qy    3180 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3256 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3315

Qy    3240 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3299
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3316 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3375

Qy    3300 ACACTTTGTTTGTAAATTAAAAAAAAAAAAAAAAA 3334
           ||| ||| |||  |||  ||||||||||||||||||
Db    3376 ACATTTTTTTTTAAAAAAAAAAAAAAAAAAAAAAA 3410
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RESULT 3
US-10-123-904-37
; Sequence 37, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 37
; LENGTH: 3501
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2762, 2778
; OTHER INFORMATION: unknown base
US-10-123-904-37

Query Match 99.1%; Score 3303.4; DB 9; Length 3501;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3321; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

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Qy       1 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      76 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 135

Qy      61 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGGGAAGAACTGAGAGGCGC 120
           |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db     136 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGAGAAGAACTGAGAGGCGC 195

Qy     121 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     196 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 255

Qy     181 ACGGGACCGGAGCTTCACGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 240
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db     256 ACGGGACCGGAGCTTCATGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 315

Qy     241 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGGCCTGTGCACCAGC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     316 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGGCCTGTGCACCAGC 375

Qy     301 CTGCCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCCGGGGAGTTTCTG 360
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     376 CTGTCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCCGGGGAGTTTCTG 435

Qy     361 GATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     436 GATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 495

Qy     421 ATTCGGTTTGATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 480
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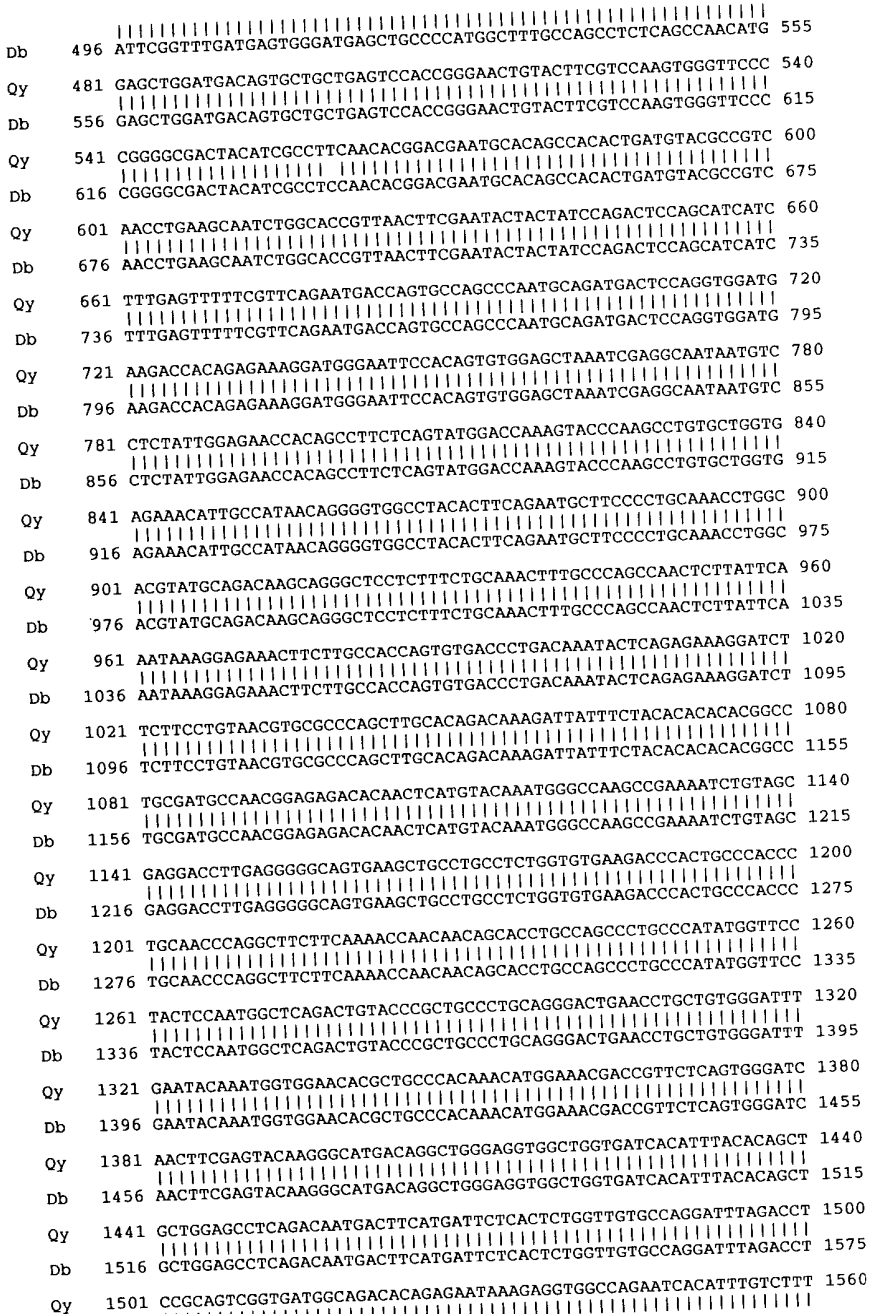
Db 496 ATTCGGTTTGATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 555
Qy 481 GAGCTGGATGACAGTGCTGCTGAGTCCACCGGGAACTGTACTTCGTCCAAGTGGGTTCCC 540
Db 556 GAGCTGGATGACAGTGCTGCTGAGTCCACCGGGAACTGTACTTCGTCCAAGTGGGTTCCC 615
Qy 541 CGGGGCGACTACATCGCCTTCAACACGGACGAATGCACAGCCACACTGATGTACGCCGTC 600
Db 616 CGGGGCGACTACATCGCCTCCAACACGGACGAATGCACAGCCACACTGATGTACGCCGTC 675
Qy 601 AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATCATC 660
Db 676 AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATCATC 735
Qy 661 TTTGAGTTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGGATG 720
Db 736 TTTGAGTTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGGATG 795
Qy 721 AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 780
Db 796 AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 855
Qy 781 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 840
Db 856 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 915
Qy 841 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 900
Db 916 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 975
Qy 901 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCA 960
Db 976 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCA 1035
Qy 961 AATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1020
Db 1036 AATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1095
Qy 1021 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1080
Db 1096 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1155
Qy 1081 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1140
Db 1156 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1215
Qy 1141 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1200
Db 1216 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1275
Qy 1201 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1260
Db 1276 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1335
Qy 1261 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1320
Db 1336 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1395
Qy 1321 GAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 1380
Db 1396 GAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 1455
Qy 1381 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1440
Db 1456 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1515
Qy 1441 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTTAGACCT 1500
Db 1516 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTTAGACCT 1575
Qy 1501 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1560
Db 1576 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1635
Qy 1561 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1620
Db 1636 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1695
Qy 1621 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1680
Db 1696 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1755
Qy 1681 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1740
Db 1756 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1815
Qy 1741 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1800
Db 1816 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1875
Qy 1801 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1860
Db 1876 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1935
Qy 1861 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1920
Db 1936 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1995
Qy 1921 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 1980
Db 1996 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 2055
Qy 1981 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2040
Db 2056 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2115
Qy 2041 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2100
Db 2116 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2175
Qy 2101 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2160
Db 2176 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2235
Qy 2161 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2220
Db 2236 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2295
Qy 2221 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2280
Db 2296 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2355
Qy 2281 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2340
Db 2356 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2415
Qy 2341 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2400
Db 2416 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2475
Qy 2401 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2460
Db 2476 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2535
Qy 2461 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2520
Db 2536 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2595
Qy 2521 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2580
Db 2596 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2655
Qy 2581 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2640
Db 2656 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2715

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Qy   2641 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGAAGACTACTTACGTG 2700
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Db   2716 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGANGACTACTTACGTG 2775

Qy   2701 TGGCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2760
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2776 TGNCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2835

Qy   2761 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2836 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2895

Qy   2821 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2896 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2955

Qy   2881 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2956 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 3015

Qy   2941 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAA-TCACTC 2999
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||| |||||
Db   3016 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAAGTCACTT 3075

Qy   3000 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3059
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3076 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3135

Qy   3060 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3119
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3136 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3195

Qy   3120 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3179
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3196 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3255

Qy   3180 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3256 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3315

Qy   3240 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3299
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Db   3316 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3375

Qy   3300 ACACTTTGTTTGTAAATTAAAAAAAAAAAAAAAA 3334
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Db   3376 ACATTTTTTTTTAAAAAAAAAAAAAAAAAAAAAA 3410


RESULT 4
US-10-140-470-37
; Sequence 37, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C160
;  CURRENT APPLICATION NUMBER: US/10/140,470
;  CURRENT FILING DATE:  2002-05-06
;  Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 37
;   LENGTH: 3501
;   TYPE: DNA
;   ORGANISM: Homo Sapien
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 2762, 2778
;   OTHER INFORMATION: unknown base
US-10-140-470-37

  Query Match             99.1%;  Score 3303.4;  DB 9;  Length 3501;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 3321;  Conservative    0;  Mismatches   13;  Indels    1;  Gaps    1;

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     76 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 135

Qy     61 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGGGAAGAACTGAGAGGCGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    136 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGAGAAGAACTGAGAGGCGC 195

Qy    121 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    196 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 255

Qy    181 ACGGGACCGGAGCTTCACGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 240
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    256 ACGGGACCGGAGCTTCATGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 315

Qy    241 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGGCCTGTGCACCAGC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    316 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGGCCTGTGCACCAGC 375

Qy    301 CTGCCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCCGGGGAGTTTCTG 360
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    376 CTGTCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCCGGGGAGTTTCTG 435

Qy    361 GATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    436 GATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 495

Qy    421 ATTCGGTTTGATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    496 ATTCGGTTTGATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 555

Qy    481 GAGCTGGATGACAGTGCTGCTGAGTCCACCGGGAACTGTACTTCGTCCAAGTGGGTTCCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    556 GAGCTGGATGACAGTGCTGCTGAGTCCACCGGGAACTGTACTTCGTCCAAGTGGGTTCCC 615

Qy    541 CGGGGCGACTACATCGCCTTCAACACGGACGAATGCACAGCCACACTGATGTACGCCGTC 600
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Db    616 CGGGGCGACTACATCGCCTCCAACACGGACGAATGCACAGCCACACTGATGTACGCCGTC 675

Qy    601 AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATCATC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    676 AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATCATC 735

Qy    661 TTTGAGTTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGGATG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    736 TTTGAGTTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGGATG 795

Qy    721 AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    796 AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 855

Qy    781 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 840
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Db    856 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 915

Qy    841 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 900

Db    916 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 975

Qy    901 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCA 960

Db    976 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCA 1035

Qy    961 AATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1020

Db   1036 AATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1095

Qy   1021 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1080

Db   1096 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1155

Qy   1081 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1140

Db   1156 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1215

Qy   1141 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1200

Db   1216 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1275

Qy   1201 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1260

Db   1276 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1335

Qy   1261 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1320

Db   1336 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1395

Qy   1321 GAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 1380

Db   1396 GAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 1455

Qy   1381 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1440

Db   1456 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1515

Qy   1441 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTTAGACCT 1500

Db   1516 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTTAGACCT 1575

Qy   1501 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1560

Db   1576 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1635

Qy   1561 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1620

Db   1636 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1695

Qy   1621 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1680

Db   1696 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1755

Qy   1681 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1740

Db   1756 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1815

Qy   1741 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1800

Db   1816 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1875

Qy   1801 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1860

Db   1876 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1935

Qy   1861 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1920

Db   1936 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1995

Qy   1921 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 1980

Db   1996 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 2055

Qy   1981 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2040

Db   2056 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2115

Qy   2041 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2100

Db   2116 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2175

Qy   2101 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2160

Db   2176 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2235

Qy   2161 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2220

Db   2236 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2295

Qy   2221 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2280

Db   2296 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2355

Qy   2281 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2340

Db   2356 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2415

Qy   2341 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2400

Db   2416 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2475

Qy   2401 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2460

Db   2476 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2535

Qy   2461 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2520

Db   2536 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2595

Qy   2521 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2580

Db   2596 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2655

Qy   2581 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2640

Db   2656 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2715

Qy   2641 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGAAGACTACTTACGTG 2700

Db   2716 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGANGACTACTTACGTG 2775

Qy   2701 TGGCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2760

Db   2776 TGNCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2835

Qy   2761 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2820

Db   2836 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2895

Qy   2821 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2880

Db   2896 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2955

Qy   2881 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 2940

Db   2956 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 3015

Qy   2941 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAA-TCACTC 2999

Db   3016 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAAGTCACTT 3075
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Qy   3000 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3059
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3076 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3059

Qy   3060 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3135
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3136 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3119

Qy   3120 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3195
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3196 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3179

Qy   3180 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3255
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3256 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3239

Qy   3240 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3315
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3316 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3299

Qy   3300 ACACTTTGTTTGTAAATTAAAAAAAAAAAAAAAAA 3334
          ||| ||| |||  ||| ||||||||||||||||
Db   3376 ACATTTTTTTTTAAAAAAAAAAAAAAAAAAAAAA 3410
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RESULT 5
US-10-175-746-37
; Sequence 37, Application US/10175746
; Publication No. US20030027270A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C353
; CURRENT APPLICATION NUMBER: US/10/175,746
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 37
; LENGTH: 3501
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2762, 2778
; OTHER INFORMATION: unknown base
US-10-175-746-37

Query Match 99.1%; Score 3303.4; DB 9; Length 3501;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3321; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

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Qy      1 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     76 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 135

Qy     61 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGGGAAGAACTGAGAGGCGC 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    136 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGAGAAGAACTGAGAGGCGC 195

Qy    121 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    196 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 255

Qy    181 ACGGGACCGGAGCTTCACGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 240
          ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    256 ACGGGACCGGAGCTTCATGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 315

Qy    241 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGGCCTGTGCACCAGC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    316 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGGCCTGTGCACCAGC 375

Qy    301 CTGCCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCCGGGGAGTTTCTG 360
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    376 CTGTCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCCGGGGAGTTTCTG 435

Qy    361 GATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    436 GATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 495

Qy    421 ATTCGGTTTGATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    496 ATTCGGTTTGATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 555

Qy    481 GAGCTGGATGACAGTGCTGCTGAGTCCACCGGGAACTGTACTTCGTCCAAGTGGGTTCCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    556 GAGCTGGATGACAGTGCTGCTGAGTCCACCGGGAACTGTACTTCGTCCAAGTGGGTTCCC 615

Qy    541 CGGGGCGACTACATCGCCTTCAACACGGACGAATGCACAGCCACACTGATGTACGCCGTC 600
          ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db    616 CGGGGCGACTACATCGCCTCCAACACGGACGAATGCACAGCCACACTGATGTACGCCGTC 675

Qy    601 AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATCATC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    676 AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATCATC 735

Qy    661 TTTGAGTTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGGATG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    736 TTTGAGTTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGGATG 795

Qy    721 AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    796 AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 855

Qy    781 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    856 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 915

Qy    841 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    916 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 975

Qy    901 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    976 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCA 1035

Qy    961 AATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1036 AATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1095

Qy   1021 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1096 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1155

Qy   1081 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1156 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1215

Qy   1141 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1200
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1216 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1275

Qy       1201 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1276 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1335

Qy       1261 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1336 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1395

Qy       1321 GAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1396 GAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 1455

Qy       1381 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1456 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1515

Qy       1441 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTTAGACCT 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1516 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTTAGACCT 1575

Qy       1501 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1576 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1635

Qy       1561 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1636 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1695

Qy       1621 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1696 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1755

Qy       1681 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1756 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1815

Qy       1741 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1816 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1875

Qy       1801 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1876 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1935

Qy       1861 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1936 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1995

Qy       1921 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1996 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 2055

Qy       1981 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2056 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2115

Qy       2041 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2116 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2175

Qy       2101 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2176 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2235

Qy       2161 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2236 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2295

Qy       2221 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2296 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2355

Qy       2281 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2356 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2415

Qy       2341 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2416 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2475

Qy       2401 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2476 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2535

Qy       2461 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2536 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2595

Qy       2521 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2580
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2596 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2655

Qy       2581 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2640
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2656 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2715

Qy       2641 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGAAGACTACTTACGTG 2700
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db       2716 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGANGACTACTTACGTG 2775

Qy       2701 TGGCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2760
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2776 TGNCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2835

Qy       2761 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2820
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2836 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2895

Qy       2821 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2896 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2955

Qy       2881 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 2940
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2956 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 3015

Qy       2941 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAA-TCACTC 2999
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||| 
Db       3016 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAAGTCACTT 3075

Qy       3000 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3059
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3076 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3135

Qy       3060 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3136 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3195

Qy       3120 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3196 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3255

Qy       3180 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3256 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3315

Qy       3240 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3316 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3375

Qy       3300 ACACTTTGTTTGTAAATTAAAAAAAAAAAAAAAAA 3334
              ||| ||| |||  |||  |||||||||||||||||
Db       3376 ACATTTTTTTTAAAAAAAAAAAAAAAAAAAAAAAA 3410
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RESULT 6
US-10-176-918-37
; Sequence 37, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C382
;  CURRENT APPLICATION NUMBER: US/10/176,918
;  CURRENT FILING DATE:  2002-06-20
;     Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 37
;   LENGTH: 3501
;   TYPE: DNA
;   ORGANISM: Homo Sapien
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 2762, 2778
;   OTHER INFORMATION: unknown base
US-10-176-918-37

  Query Match             99.1%;  Score 3303.4;  DB 9;  Length 3501;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 3321;  Conservative    0;  Mismatches   13;  Indels    1;  Gaps    1;

Qy       1 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      76 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 135

Qy      61 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGGGAAGAACTGAGAGGCGC 120
          ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     136 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGAGAAGAACTGAGAGGCGC 195

Qy     121 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     196 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 255

Qy     181 ACGGGACCGGAGCTTCACGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 240
          |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db     256 ACGGGACCGGAGCTTCATGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 315

Qy     241 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGGCCTGTGCACCAGC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     316 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGGCCTGTGCACCAGC 375

Qy     301 CTGCCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCCGGGGAGTTTCTG 360
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     376 CTGTCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCCGGGGAGTTTCTG 435

Qy     361 GATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     436 GATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 495

Qy     421 ATTCGGTTTGATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     496 ATTCGGTTTGATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 555

Qy     481 GAGCTGGATGACAGTGCTGCTGAGTCCACCGGGAACTGTACTTCGTCCAAGTGGGTTCCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     556 GAGCTGGATGACAGTGCTGCTGAGTCCACCGGGAACTGTACTTCGTCCAAGTGGGTTCCC 615

Qy     541 CGGGGCGACTACATCGCCTTCAACACGGACGAATGCACAGCCACACTGATGTACGCCGTC 600
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     616 CGGGGCGACTACATCGCCTCCAACACGGACGAATGCACAGCCACACTGATGTACGCCGTC 675

Qy     601 AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATCATC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     676 AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATCATC 735

Qy     661 TTTGAGTTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGGATG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     736 TTTGAGTTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGGATG 795

Qy     721 AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     796 AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 855

Qy     781 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     856 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 915

Qy     841 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     916 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 975

Qy     901 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     976 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCA 1035

Qy     961 AATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1036 AATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1095

Qy    1021 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1096 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1155

Qy    1081 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1156 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1215

Qy    1141 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1216 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1275

Qy    1201 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1276 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1335

Qy    1261 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1336 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1395

Qy    1321 GAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1396 GAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 1455

Qy    1381 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1456 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1515

Qy    1441 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTTAGACCT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1516 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTTAGACCT 1575

Qy    1501 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1560
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Db   1576 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1635
Qy   1561 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1620
Db   1636 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1695
Qy   1621 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1680
Db   1696 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1755
Qy   1681 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1740
Db   1756 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1815
Qy   1741 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1800
Db   1816 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1875
Qy   1801 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1860
Db   1876 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1935
Qy   1861 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1920
Db   1936 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1995
Qy   1921 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 1980
Db   1996 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 2055
Qy   1981 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2040
Db   2056 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2115
Qy   2041 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2100
Db   2116 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2175
Qy   2101 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2160
Db   2176 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2235
Qy   2161 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2220
Db   2236 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2295
Qy   2221 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2280
Db   2296 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2355
Qy   2281 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2340
Db   2356 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2415
Qy   2341 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2400
Db   2416 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2475
Qy   2401 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2460
Db   2476 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2535
Qy   2461 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2520
Db   2536 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2595
Qy   2521 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2580
Db   2596 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2655
Qy   2581 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2640
Db   2656 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2715
Qy   2641 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGAAGACTACTTACGTG 2700
Db   2716 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGANGACTACTTACGTG 2775
Qy   2701 TGGCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2760
Db   2776 TGNCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2835
Qy   2761 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2820
Db   2836 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2895
Qy   2821 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2880
Db   2896 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2955
Qy   2881 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 2940
Db   2956 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 3015
Qy   2941 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAA-TCACTC 2999
Db   3016 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAAGTCACTT 3075
Qy   3000 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3059
Db   3076 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3135
Qy   3060 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3119
Db   3136 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3195
Qy   3120 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3179
Db   3196 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3255
Qy   3180 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3239
Db   3256 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3315
Qy   3240 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3299
Db   3316 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3375
Qy   3300 ACACTTTGTTTGTAAATTAAAAAAAAAAAAAAAAA 3334
Db   3376 ACATTTTTTTTTAAAAAAAAAAAAAAAAAAAAAAA 3410
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RESULT 7
US-10-176-921-37
; Sequence 37, Application US/10176921
; Publication No. US20030027276A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin

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;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C288
;  CURRENT APPLICATION NUMBER: US/10/176,921
;  CURRENT FILING DATE:  2002-06-20
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 37
;   LENGTH: 3501
;   TYPE: DNA
;   ORGANISM: Homo Sapien
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 2762, 2778
;   OTHER INFORMATION: unknown base
US-10-176-921-37

  Query Match             99.1%;  Score 3303.4;  DB 9;  Length 3501;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 3321;  Conservative    0;  Mismatches   13;  Indels    1;  Gaps    1;

Qy       1 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 60
Db      76 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 135

Qy      61 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGGGAAGAACTGAGAGGCGC 120
Db     136 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGAGAAGAACTGAGAGGCGC 195

Qy     121 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 180
Db     196 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 255

Qy     181 ACGGGACCGGAGCTTCACGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 240
Db     256 ACGGGACCGGAGCTTCATGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 315

Qy     241 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGGCCTGTGCACCAGC 300
Db     316 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGGCCTGTGCACCAGC 375

Qy     301 CTGCCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCCGGGGAGTTTCTG 360
Db     376 CTGTCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCCGGGGAGTTTCTG 435

Qy     361 GATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 420
Db     436 GATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 495

Qy     421 ATTCGGTTTGATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 480
Db     496 ATTCGGTTTGATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 555

Qy     481 GAGCTGGATGACAGTGCTGCTGAGTCCACCGGGAACTGTACTTCGTCCAAGTGGGTTCCC 540
Db     556 GAGCTGGATGACAGTGCTGCTGAGTCCACCGGGAACTGTACTTCGTCCAAGTGGGTTCCC 615

Qy     541 CGGGGCGACTACATCGCCTTCAACACGGACGAATGCACAGCCACACTGATGTACGCCGTC 600
Db     616 CGGGGCGACTACATCGCCTCCAACACGGACGAATGCACAGCCACACTGATGTACGCCGTC 675

Qy     601 AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATCATC 660
Db     676 AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATCATC 735

Qy     661 TTTGAGTTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGGATG 720
Db     736 TTTGAGTTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGGATG 795

Qy     721 AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 780
Db     796 AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 855

Qy     781 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 840
Db     856 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 915

Qy     841 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 900
Db     916 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 975

Qy     901 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCA 960
Db     976 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCA 1035

Qy     961 AATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1020
Db    1036 AATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1095

Qy    1021 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1080
Db    1096 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1155

Qy    1081 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1140
Db    1156 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1215

Qy    1141 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1200
Db    1216 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1275

Qy    1201 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1260
Db    1276 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1335

Qy    1261 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1320
Db    1336 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1395

Qy    1321 GAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 1380
Db    1396 GAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 1455

Qy    1381 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1440
Db    1456 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1515

Qy    1441 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTTAGACCT 1500
Db    1516 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTTAGACCT 1575

Qy    1501 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1560
Db    1576 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1635

Qy    1561 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1620
Db    1636 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1695

Qy    1621 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1680
Db    1696 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1755

Qy    1681 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1740
Db    1756 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1815

Qy    1741 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1800
Db    1816 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1875

Qy    1801 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1860
Db    1876 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1935

Qy    1861 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1920
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Db   1936 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1995

Qy   1921 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 1980

Db   1996 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 2055

Qy   1981 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2040

Db   2056 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2115

Qy   2041 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2100

Db   2116 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2175

Qy   2101 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2160

Db   2176 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2235

Qy   2161 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2220

Db   2236 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2295

Qy   2221 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2280

Db   2296 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2355

Qy   2281 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2340

Db   2356 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2415

Qy   2341 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2400

Db   2416 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2475

Qy   2401 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2460

Db   2476 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2535

Qy   2461 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2520

Db   2536 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2595

Qy   2521 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2580

Db   2596 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2655

Qy   2581 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2640

Db   2656 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2715

Qy   2641 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGAAGACTACTTACGTG 2700

Db   2716 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGANGACTACTTACGTG 2775

Qy   2701 TGGCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2760

Db   2776 TGNCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2835

Qy   2761 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2820

Db   2836 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2895

Qy   2821 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2880

Db   2896 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2955

Qy   2881 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 2940

Db   2956 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 3015

Qy   2941 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAA-TCACTC 2999

Db   3016 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAAGTCACTT 3075

Qy   3000 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3059

Db   3076 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3135

Qy   3060 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3119

Db   3136 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3195

Qy   3120 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3179

Db   3196 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3255

Qy   3180 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3239

Db   3256 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3315

Qy   3240 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3299

Db   3316 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3375

Qy   3300 ACACTTTGTTTGTAAATTAAAAAAAAAAAAAAAAA 3334

Db   3376 ACATTTTTTTTTAAAAAAAAAAAAAAAAAAAAAAA 3410
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RESULT 8
US-10-137-865-37
; Sequence 37, Application US/10137865
; Publication No. US20030032155A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C154
; CURRENT APPLICATION NUMBER: US/10/137,865
; CURRENT FILING DATE: 2002-05-03
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 37
; LENGTH: 3501
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2762, 2778
; OTHER INFORMATION: unknown base
US-10-137-865-37

Query Match 99.1%; Score 3303.4; DB 9; Length 3501;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3321; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

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Qy      1 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 60

Db     76 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 135
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Qy      61 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGGGAAGAACTGAGAGGCGC 120
           ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db     136 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGAGAAGAACTGAGAGGCGC 195

Qy     121 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     196 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 255

Qy     181 ACGGGACCGGAGCTTCACGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 240
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     256 ACGGGACCGGAGCTTCATGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 315

Qy     241 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGGCCTGTGCACCAGC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     316 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGGCCTGTGCACCAGC 375

Qy     301 CTGCCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCCGGGGAGTTTCTG 360
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     376 CTGTCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCCGGGGAGTTTCTG 435

Qy     361 GATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     436 GATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 495

Qy     421 ATTCGGTTTGATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     496 ATTCGGTTTGATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 555

Qy     481 GAGCTGGATGACAGTGCTGCTGAGTCCACCGGGAACTGTACTTCGTCCAAGTGGGTTCCC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     556 GAGCTGGATGACAGTGCTGCTGAGTCCACCGGGAACTGTACTTCGTCCAAGTGGGTTCCC 615

Qy     541 CGGGGCGACTACATCGCCTTCAACACGGACGAATGCACAGCCACACTGATGTACGCCGTC 600
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db     616 CGGGGCGACTACATCGCCTCCAACACGGACGAATGCACAGCCACACTGATGTACGCCGTC 675

Qy     601 AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATCATC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     676 AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATCATC 735

Qy     661 TTTGAGTTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGGATG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     736 TTTGAGTTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGGATG 795

Qy     721 AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     796 AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 855

Qy     781 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     856 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 915

Qy     841 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     916 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 975

Qy     901 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCA 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     976 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCA 1035

Qy     961 AATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1036 AATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1095

Qy    1021 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1096 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1155

Qy    1081 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1140
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Db    1156 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1215

Qy    1141 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1216 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1275

Qy    1201 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1276 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1335

Qy    1261 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1336 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1395

Qy    1321 GAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 1380
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Db    1396 GAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 1455

Qy    1381 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1456 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1515

Qy    1441 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTTAGACCT 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1516 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTTAGACCT 1575

Qy    1501 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1560
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1576 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1635

Qy    1561 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1620
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1636 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1695

Qy    1621 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1680
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1696 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1755

Qy    1681 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1740
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Db    1756 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1815

Qy    1741 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1800
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Db    1816 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1875

Qy    1801 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1876 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1935

Qy    1861 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1936 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1995

Qy    1921 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1996 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 2055

Qy    1981 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2040
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Db    2056 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2115

Qy    2041 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2100
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Db    2116 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2175

Qy    2101 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2176 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2235

Qy    2161 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2236 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2295

Qy    2221 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2280
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2296 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2355

Qy    2281 GTCATCATCCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2340
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2356 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2415

Qy    2341 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2400
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2416 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2475

Qy    2401 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2460
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2476 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2535

Qy    2461 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2520
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2536 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2595

Qy    2521 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2580
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2596 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2655

Qy    2581 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2640
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2656 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2715

Qy    2641 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGAAGACTACTTACGTG 2700
           ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db    2716 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGANGACTACTTACGTG 2775

Qy    2701 TGGCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2760
           || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2776 TGNCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2835

Qy    2761 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2820
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2836 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2895

Qy    2821 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2880
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2896 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2955

Qy    2881 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 2940
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2956 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 3015

Qy    2941 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAA-TCACTC 2999
           ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db    3016 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAAGTCACTT 3075

Qy    3000 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3059
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3076 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3135

Qy    3060 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3119
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Db    3136 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3195

Qy    3120 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3179
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3196 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3255

Qy    3180 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3256 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3315

Qy    3240 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3299
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    3316 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3375

Qy    3300 ACACTTTGTTTGTAAATTAAAAAAAAAAAAAAAA 3334
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Db    3376 ACATTTTTTTTTAAAAAAAAAAAAAAAAAAAAAA 3410
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RESULT 9
US-10-140-474-37
; Sequence 37, Application US/10140474
; Publication No. US20030032156A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C162
;  CURRENT APPLICATION NUMBER: US/10/140,474
;  CURRENT FILING DATE:  2002-05-06
;  Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 37
;   LENGTH: 3501
;   TYPE: DNA
;   ORGANISM: Homo Sapien
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 2762, 2778
;   OTHER INFORMATION: unknown base
US-10-140-474-37

  Query Match           99.1%;  Score 3303.4;  DB 9;  Length 3501;
  Best Local Similarity  99.6%;  Pred. No. 0;
  Matches 3321;  Conservative    0;  Mismatches   13;  Indels    1;  Gaps    1;

Qy       1 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      76 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 135

Qy      61 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGGGAAGAACTGAGAGGCGC 120
           ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db     136 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGAGAAGAACTGAGAGGCGC 195

Qy     121 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     196 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 255

Qy     181 ACGGGACCGGAGCTTCACGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 240
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db     256 ACGGGACCGGAGCTTCATGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 315

Qy     241 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGGCCTGTGCACCAGC 300
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Db     316 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGGCCTGTGCACCAGC 375

Qy     301 CTGCCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCCGGGGAGTTTCTG 360
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     376 CTGTCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCCGGGGAGTTTCTG 435

Qy     361 GATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     436 GATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 495
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Qy    421 ATTCGGTTTGATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    496 ATTCGGTTTGATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 555

Qy    481 GAGCTGGATGACAGTGCTGCTGAGTCCACCGGGAACTGTACTTCGTCCAAGTGGGTTCCC 540
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    556 GAGCTGGATGACAGTGCTGCTGAGTCCACCGGGAACTGTACTTCGTCCAAGTGGGTTCCC 615

Qy    541 CGGGGCGACTACATCGCCTTCAACACGGACGAATGCACAGCCACACTGATGTACGCCGTC 600
          |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db    616 CGGGGCGACTACATCGCCTCCAACACGGACGAATGCACAGCCACACTGATGTACGCCGTC 675

Qy    601 AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATCATC 660
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    676 AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATCATC 735

Qy    661 TTTGAGTTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGGATG 720
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    736 TTTGAGTTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGGATG 795

Qy    721 AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 780
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    796 AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 855

Qy    781 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    856 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 915

Qy    841 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    916 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 975

Qy    901 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    976 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCA 1035

Qy    961 AATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1036 AATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1095

Qy   1021 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1096 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1155

Qy   1081 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1156 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1215

Qy   1141 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1216 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1275

Qy   1201 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1276 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1335

Qy   1261 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1320
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1336 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1395

Qy   1321 GAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 1380
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1396 GAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 1455

Qy   1381 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1456 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1515

Qy   1441 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTTAGACCT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1516 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTTAGACCT 1575

Qy   1501 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1576 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1635

Qy   1561 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1636 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1695

Qy   1621 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1696 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1755

Qy   1681 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1756 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1815

Qy   1741 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1816 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1875

Qy   1801 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1876 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1935

Qy   1861 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1936 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1995

Qy   1921 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1996 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 2055

Qy   1981 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2056 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2115

Qy   2041 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2100
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Db   2116 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2175

Qy   2101 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2176 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2235

Qy   2161 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2236 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2295

Qy   2221 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2296 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2355

Qy   2281 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2356 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2415

Qy   2341 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2416 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2475

Qy   2401 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2476 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2535

Qy   2461 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2536 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2595

Qy   2521 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2596 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2655

Qy   2581 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2640
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Db   2656 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2715

Qy   2641 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGAAGACTACTTACGTG 2700

Db   2716 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGANGACTACTTACGTG 2775

Qy   2701 TGGCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2760

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Qy   2761 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2820

Db   2836 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2895

Qy   2821 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2880

Db   2896 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2955

Qy   2881 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 2940

Db   2956 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 3015

Qy   2941 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAA-TCACTC 2999

Db   3016 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAAGTCACTT 3075

Qy   3000 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3059

Db   3076 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3135

Qy   3060 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3119

Db   3136 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3195

Qy   3120 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3179

Db   3196 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3255

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Db   3256 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3315

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Db   3316 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3375

Qy   3300 ACACTTTGTTTGTAAATTAAAAAAAAAAAAAAAAA 3334

Db   3376 ACATTTTTTTTTAAAAAAAAAAAAAAAAAAAAAAA 3410
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RESULT 10
US-10-142-431-37
; Sequence 37, Application US/10142431
; Publication No. US20030036179A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C251
; CURRENT APPLICATION NUMBER: US/10/142,431
; CURRENT FILING DATE: 2002-05-10
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 37
; LENGTH: 3501
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2762, 2778
; OTHER INFORMATION: unknown base
US-10-142-431-37

Query Match 99.1%; Score 3303.4; DB 9; Length 3501;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3321; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

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Qy      1 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 60

Db     76 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 135

Qy     61 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGGGAAGAACTGAGAGGCGC 120

Db    136 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGAGAAGAACTGAGAGGCGC 195

Qy    121 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 180

Db    196 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 255

Qy    181 ACGGGACCGGAGCTTCACGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 240

Db    256 ACGGGACCGGAGCTTCATGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 315

Qy    241 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGGCCTGTGCACCAGC 300

Db    316 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGGCCTGTGCACCAGC 375

Qy    301 CTGCCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCCGGGGAGTTTCTG 360

Db    376 CTGTCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCCGGGGAGTTTCTG 435

Qy    361 GATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 420

Db    436 GATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 495

Qy    421 ATTCGGTTTGATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 480

Db    496 ATTCGGTTTGATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 555

Qy    481 GAGCTGGATGACAGTGCTGCTGAGTCCACCGGGAACTGTACTTCGTCCAAGTGGGTTCCC 540

Db    556 GAGCTGGATGACAGTGCTGCTGAGTCCACCGGGAACTGTACTTCGTCCAAGTGGGTTCCC 615

Qy    541 CGGGGCGACTACATCGCCTTCAACACGGACGAATGCACAGCCACACTGATGTACGCCGTC 600

Db    616 CGGGGCGACTACATCGCCTCCAACACGGACGAATGCACAGCCACACTGATGTACGCCGTC 675

Qy    601 AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATCATC 660

Db    676 AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATCATC 735

Qy    661 TTTGAGTTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGGATG 720

Db    736 TTTGAGTTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGGATG 795

Qy    721 AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 780

Db    796 AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 855
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Qy    781 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 840
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    856 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 915

Qy    841 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    916 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 975

Qy    901 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCA 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    976 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCA 1035

Qy    961 AATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1036 AATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1095

Qy   1021 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1080
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1096 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1155

Qy   1081 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1140
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1156 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1215

Qy   1141 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1200
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1216 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1275

Qy   1201 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1276 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1335

Qy   1261 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1320
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Db   1336 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1395

Qy   1321 GAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 1380
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Db   1396 GAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 1455

Qy   1381 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1456 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1515

Qy   1441 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTTAGACCT 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1516 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTTAGACCT 1575

Qy   1501 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1576 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1635

Qy   1561 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1636 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1695

Qy   1621 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1696 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1755

Qy   1681 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1756 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1815

Qy   1741 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1816 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1875

Qy   1801 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1876 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1935

Qy   1861 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1936 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1995

Qy   1921 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1996 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 2055

Qy   1981 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2056 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2115

Qy   2041 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2100
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Db   2116 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2175

Qy   2101 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2176 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2235

Qy   2161 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2236 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2295

Qy   2221 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2280
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Db   2296 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2355

Qy   2281 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2340
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Db   2356 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2415

Qy   2341 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2416 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2475

Qy   2401 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2460
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Db   2476 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2535

Qy   2461 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2520
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Db   2536 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2595

Qy   2521 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2596 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2655

Qy   2581 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2640
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Db   2656 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2715

Qy   2641 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGAAGACTACTTACGTG 2700
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   2716 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGANGACTACTTACGTG 2775

Qy   2701 TGGCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2760
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2776 TGNCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2835

Qy   2761 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2836 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2895

Qy   2821 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2896 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2955

Qy   2881 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2956 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 3015

Qy   2941 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAA-TCACTC 2999
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Db   3016 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAAGTCACTT 3075

Qy   3000 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3059

Db   3076 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3135

Qy   3060 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3119

Db   3136 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3195

Qy   3120 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3179

Db   3196 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3255

Qy   3180 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3239

Db   3256 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3315

Qy   3240 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3299

Db   3316 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3375

Qy   3300 ACACTTTGTTTGTAAATTAAAAAAAAAAAAAAAA 3334

Db   3376 ACATTTTTTTTTAAAAAAAAAAAAAAAAAAAAAA 3410
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RESULT 11
US-10-143-114-37
; Sequence 37, Application US/10143114
; Publication No. US20030036180A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Beresini,Maureen
; APPLICANT: DeForge,Laura
; APPLICANT: Desnoyers,Luc
; APPLICANT: Filvaroff,Ellen
; APPLICANT: Gao,Wei-Qiang
; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Sherwood,Steven
; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C211
; CURRENT APPLICATION NUMBER: US/10/143,114
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 37
; LENGTH: 3501
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 2762, 2778
; OTHER INFORMATION: unknown base
US-10-143-114-37

Query Match 99.1%; Score 3303.4; DB 9; Length 3501;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 3321; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

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Qy      1 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 60

Db     76 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 135

Qy     61 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGGGAAGAACTGAGAGGCGC 120

Db    136 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGAGAAGAACTGAGAGGCGC 195

Qy    121 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 180

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Db   1036 AATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1095

Qy   1021 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1080

Db   1096 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1155

Qy   1081 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1140

Db   1156 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1215
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Qy   1141 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1200
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Qy   1201 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1260
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Db   1276 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1335

Qy   1261 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1320
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Db   1396 GAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 1455

Qy   1381 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1440
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Db   1456 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1515

Qy   1441 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTTAGACCT 1500
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Qy   1501 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1560
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Db   1576 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1635

Qy   1561 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1620
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Db   1636 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1695

Qy   1621 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1680
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Db   1696 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1755

Qy   1681 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1756 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1815

Qy   1741 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1816 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1875

Qy   1801 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1876 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1935

Qy   1861 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1936 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1995

Qy   1921 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1996 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 2055

Qy   1981 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2056 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2115

Qy   2041 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2116 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2175

Qy   2101 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2176 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2235

Qy   2161 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2236 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2295

Qy   2221 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2296 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2355

Qy   2281 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2356 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2415

Qy   2341 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2416 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2475

Qy   2401 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2476 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2535

Qy   2461 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2536 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2595

Qy   2521 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2596 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2655

Qy   2581 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2656 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2715

Qy   2641 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGAAGACTACTTACGTG 2700
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2716 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGANGACTACTTACGTG 2775

Qy   2701 TGGCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2760
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2776 TGNCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2835

Qy   2761 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2836 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2895

Qy   2821 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2896 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2955

Qy   2881 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2956 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 3015

Qy   2941 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAA-TCACTC 2999
          ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db   3016 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAAGTCACTT 3075

Qy   3000 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3059
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3076 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3135

Qy   3060 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3119
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3136 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3195

Qy   3120 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3179
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3196 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3255

Qy   3180 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3256 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3315

Qy   3240 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3299
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3316 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3375

Qy   3300 ACACTTTGTTTGTAAATTAAAAAAAAAAAAAAAAA 3334
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Db   3376 ACATTTTTTTTTAAAAAAAAAAAAAAAAAAAAAAA 3410


RESULT 12
US-10-140-002-37
; Sequence 37, Application US/10140002
; Publication No. US20030037623A1
; GENERAL INFORMATION:
;  APPLICANT: Baker,Kevin P.
;  APPLICANT:  Beresini,Maureen
;  APPLICANT:  DeForge,Laura
;  APPLICANT:  Desnoyers,Luc
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gao,Wei-Qiang
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Sherwood,Steven
;  APPLICANT:  Smith,Victoria
;  APPLICANT:  Stewart,Timothy A.
;  APPLICANT:  Tumas,Daniel
;  APPLICANT:  Watanabe,Colin K
;  APPLICANT:  Wood,William
;  APPLICANT:  Zhang, Zemin
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3330R1C59
;  CURRENT APPLICATION NUMBER: US/10/140,002
;  CURRENT FILING DATE:  2002-05-06
;  Prior Application removed - See Palm or File Wrapper
;  NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 37
;   LENGTH: 3501
;   TYPE: DNA
;   ORGANISM: Homo Sapien
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 2762, 2778
;   OTHER INFORMATION: unknown base
US-10-140-002-37

  Query Match             99.1%;  Score 3303.4;  DB 9;  Length 3501;
  Best Local Similarity   99.6%;  Pred. No. 0;
  Matches 3321;  Conservative    0;  Mismatches   13;  Indels    1;  Gaps    1;

Qy       1 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      76 GCAGAAGCAGCAGCCGCAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 135

Qy      61 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGGGAAGAACTGAGAGGCGC 120
           |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db     136 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGAGAAGAACTGAGAGGCGC 195

Qy     121 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     196 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 255

Qy     181 ACGGGACCGGAGCTTCACGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 240
           |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db     256 ACGGGACCGGAGCTTCATGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 315

Qy     241 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGGCCTGTGCACCAGC 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     316 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGGCCTGTGCACCAGC 375

Qy     301 CTGCCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCCGGGGAGTTTCTG 360
           ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     376 CTGTCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCCGGGGAGTTTCTG 435

Qy     361 GATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db     436 GATATGAAGGACCAGTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 495

Qy     421 ATTCGGTTTGATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     496 ATTCGGTTTGATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 555

Qy     481 GAGCTGGATGACAGTGCTGCTGAGTCCACCGGGAACTGTACTTCGTCCAAGTGGGTTCCC 540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     556 GAGCTGGATGACAGTGCTGCTGAGTCCACCGGGAACTGTACTTCGTCCAAGTGGGTTCCC 615

Qy     541 CGGGGCGACTACATCGCCTTCAACACGGACGAATGCACAGCCACACTGATGTACGCCGTC 600
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     616 CGGGGCGACTACATCGCCTCCAACACGGACGAATGCACAGCCACACTGATGTACGCCGTC 675

Qy     601 AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATCATC 660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     676 AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATCATC 735

Qy     661 TTTGAGTTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGGATG 720
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     736 TTTGAGTTTTTCGTTCAGAATGACCAGTGCCAGCCCAATGCAGATGACTCCAGGTGGATG 795

Qy     721 AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     796 AAGACCACAGAGAAAGGATGGGAATTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 855

Qy     781 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     856 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 915

Qy     841 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     916 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 975

Qy     901 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCA 960
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     976 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCA 1035

Qy     961 AATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1036 AATAAAGGAGAAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1095

Qy    1021 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1096 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1155

Qy    1081 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1156 TGCGATGCCAACGGAGAGACACAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1215

Qy    1141 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1216 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1275

Qy    1201 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1276 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1335

Qy    1261 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1320
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1336 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1395

Qy    1321 GAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 1380
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1396 GAATACAAATGGTGGAACACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATC 1455

Qy    1381 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1440
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1456 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1515

Qy    1441 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTTAGACCT 1500
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1516 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTTAGACCT 1575
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Qy   1501 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1560
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1576 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1635

Qy   1561 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1620
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1636 GAGACCCTCTGTTCTGTGAACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1695

Qy   1621 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1680
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1696 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1755

Qy   1681 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1740
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1756 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1815

Qy   1741 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1800
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1816 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1875

Qy   1801 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1860
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1876 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1935

Qy   1861 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1920
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1936 TGCACCTCTTGTCCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1995

Qy   1921 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 1980
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1996 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 2055

Qy   1981 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2040
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2056 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2115

Qy   2041 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2100
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2116 CGCAACACTCCAACCAGGACTTTCAACTACAACTTCTCCGCTTTGGCAAACACCGTCACT 2175

Qy   2101 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2160
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2176 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 2235

Qy   2161 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2220
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2236 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2295

Qy   2221 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2280
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2296 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 2355

Qy   2281 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2340
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2356 GTCATCATCCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2415

Qy   2341 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2400
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2416 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2475

Qy   2401 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2460
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2476 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2535

Qy   2461 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2520
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2536 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2595

Qy   2521 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2580
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2596 CCACAGAAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2655

Qy   2581 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2640
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2656 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 2715

Qy   2641 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGAAGACTACTTACGTG 2700
          |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db   2716 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGANGACTACTTACGTG 2775

Qy   2701 TGGCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2760
          || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2776 TGNCGAGAACCCAAGCTATGCTCTGGTGGCATTTCTCTGCCTGAGCAGAGAGTCACCATC 2835

Qy   2761 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2820
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2836 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2895

Qy   2821 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2880
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2896 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAACTAGAGTACAAGTAC 2955

Qy   2881 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 2940
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   2956 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 3015

Qy   2941 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAA-TCACTC 2999
          |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||| |
Db   3016 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAAGTCACTT 3075

Qy   3000 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3059
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3076 TTTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCG 3135

Qy   3060 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3119
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3136 CTGAAGACATCCTCAGGAGGCCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCT 3195

Qy   3120 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3179
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3196 GCCTCCTCACCTTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTG 3255

Qy   3180 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3239
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3256 CAACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTTCAGATC 3315

Qy   3240 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3299
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   3316 TTTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCC 3375

Qy   3300 ACACTTTGTTTGTAAATTAAAAAAAAAAAAAAAAA 3334
          ||| ||| ||| ||| |||||||||||||||||
Db   3376 ACATTTTTTTTTAAAAAAAAAAAAAAAAAAAAAA 3410
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RESULT 13
US-09-925-299-209
; Sequence 209, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 209
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens

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;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (10)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (25)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (26)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (600)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-209

  Query Match             16.5%;  Score 551;  DB 9;  Length 625;
  Best Local Similarity   97.1%;  Pred. No. 1.2e-153;
  Matches  596;  Conservative    5;  Mismatches    8;  Indels    5;  Gaps    4;

Qy   2050 CCAACCAGGACTTTCAACTACAACTTCTCCGCTTT-GGCAAACACCGTCACTCTTGCTGG 2108
          ||||||   |  |||||||||||||||||||||| ||||||||||||||||||||||||
Db     15 CCAACCTTCANNTTCAACTACAACTTCTCCGCTTTGGGCAAACACCGTCACTCTTGCTGG 74

Qy   2109 AGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTCAGTCTCTG 2168
          |||  ||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db     75 AGG--CAAGCTTCA-TTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTCAGTCTCTG 131

Qy   2169 TGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTCCGGATTCC 2228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    132 TGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTCCGGATTCC 191

Qy   2229 TGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCAGTCATCAT 2288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    192 TGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCAGTCATCAT 251

Qy   2289 CCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGCCTTGCTGA 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    252 CCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGCCTTGCTGA 311

Qy   2349 TCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCAGCTGAACT 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    312 TCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCAGCTGAACT 371

Qy   2409 TTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCCAATGATGT 2468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    372 TTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCCAATGATGT 431

Qy   2469 GACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGTCCACAGAA 2528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    432 GACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGTCCACAGAA 491

Qy   2529 AACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGTGATGGCTG 2588
          ||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||
Db    492 AACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGAMCTGTGATGGCTG 551

Qy   2589 CAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTGGCTGACTA 2648
          |||||||||||||||||| | :| :|:||:|||||||||||||||| ||||||||||
Db    552 CAACTTCCACTTCCTGTGGGAAAAMG-SGSTGSTTGCCCGCTCTGCTCANTGGCTGACTA 610

Qy   2649 CCATGCTATCGTCA 2662
          ||||||||||||||
Db    611 CCATGCTATCGTCA 624


RESULT 14
US-09-925-299-209
; Sequence 209, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA102
;  CURRENT APPLICATION NUMBER: US/09/925,299
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05883
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1556
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 209
;   LENGTH: 625
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (10)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (25)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (26)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (600)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-209

  Query Match             16.5%;  Score 551;  DB 10;  Length 625;
  Best Local Similarity   97.1%;  Pred. No. 1.2e-153;
  Matches  596;  Conservative    5;  Mismatches    8;  Indels    5;  Gaps    4;

Qy   2050 CCAACCAGGACTTTCAACTACAACTTCTCCGCTTT-GGCAAACACCGTCACTCTTGCTGG 2108
          ||||||   |  |||||||||||||||||||||| ||||||||||||||||||||||||
Db     15 CCAACCTTCANNTTCAACTACAACTTCTCCGCTTTGGGCAAACACCGTCACTCTTGCTGG 74

Qy   2109 AGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTCAGTCTCTG 2168
          |||  ||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db     75 AGG--CAAGCTTCA-TTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTCAGTCTCTG 131

Qy   2169 TGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTCCGGATTCC 2228
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    132 TGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTCCGGATTCC 191

Qy   2229 TGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCAGTCATCAT 2288
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    192 TGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCAGTCATCAT 251

Qy   2289 CCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGCCTTGCTGA 2348
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    252 CCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGCCTTGCTGA 311

Qy   2349 TCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCAGCTGAACT 2408
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    312 TCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCAGCTGAACT 371

Qy   2409 TTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCCAATGATGT 2468
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    372 TTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCCAATGATGT 431

Qy   2469 GACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGTCCACAGAA 2528
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    432 GACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGTCCACAGAA 491

Qy   2529 AACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGTGATGGCTG 2588
          ||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||
Db    492 AACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGAMCTGTGATGGCTG 551

Qy   2589 CAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTGGCTGACTA 2648
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Db     552 CAACTTCCACTTCCTGTGGGAAAAMG-SGSTGSTTGCCCGCTCTGCTCANTGGCTGACTA 610

Qy    2649 CCATGCTATCGTCA 2662
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Db     611 CCATGCTATCGTCA 624


RESULT 15
US-10-002-050-19
; Sequence 19, Application US/10002050
; Publication No. US20030032095A1
; GENERAL INFORMATION:
;  APPLICANT: Shimkets, Richard
;  APPLICANT:  Fernandes, Elma
;  APPLICANT:  Vernet, Corine
;  APPLICANT:  Yang, Meijia
;  APPLICANT:  Boldog, Ferenc
;  APPLICANT:  Herrmann, John
;  TITLE OF INVENTION: No. US20030032095A1el Nucleic Acid Sequences Encoding Human Semap
;  FILE REFERENCE: 15966-554 Cura-54 CON-S14
;  CURRENT APPLICATION NUMBER: US/10/002,050
;  CURRENT FILING DATE:  2001-11-02
;  PRIOR APPLICATION NUMBER: 09/604,286
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: 60/140,584
;  PRIOR FILING DATE: 1999-06-23
;  NUMBER OF SEQ ID NOS: 49
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 1737
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (296)..(1687)
;   NAME/KEY: variation
;   LOCATION: (1)..(1737)
;   OTHER INFORMATION: N may be any nucleotide
US-10-002-050-19

  Query Match           16.1%;  Score 537.6;  DB 9;  Length 1737;
  Best Local Similarity  62.0%;  Pred. No. 2.3e-149;
  Matches  957;  Conservative    0;  Mismatches  569;  Indels   18;  Gaps    6;

Qy     214 GAGTACCACTATGAGTACACGGCGTGTGACAGCACGGGTTCCAGGTGGAGGGTCGCCGTG 273
           || || |||| ||| || |||| ||||| |||| || ||||||||||| || ||| |
Db     146 GATTATCACTTTGAATATACGGAATGTGATAGCAGTGGCTCCAGGTGGAGAGTTGCCATT 205

Qy     274 CCGCATACCCCGGGCCTGTGCACCAGCCTGCCTGACCCCGTCAAGGGCACCGAGTGCTCC 333
           ||  || | | |     ||| |  |||||||||||||| || |  |||| || ||| |
Db     206 CCAAATTCTGCAGTGGACTGCTCTGGCCTGCCTGACCCAGTGAGAGGCAAAGAATGCACT 265

Qy     334 TTCTCCTGCAACGCCGGGGAGTTTCTGGATATGAAGGACCAGTCATGTAAGCCATGCGCT 393
           ||||||||     | || |||| ||| || |||||| |||||  ||| |     || | |
Db     266 TTCTCCTGTGCTTCTGGAGAGTATCTAGAAATGAAGAACCAGGTATGCAGTAAGTGTGGT 325

Qy     394 GAGGGCCGCTACTCCCTCGGCACAGGCATTCGGTTTGATGAGTGGGATGAGCTGCCCCAT 453
           || |||  ||| ||| | ||||  |||||    |||||||| |||||||| ||||
Db     326 GAAGGCACCTATTCCTTGGGCAGTGGCATCAAATTTGATGAATGGGATGAATTGCCGGCA 385

Qy     454 GGCTTTGCCAGCCTCTCAGCCAACATGGAGCTGGATGACAGTGCTGCTGAGTCCA---CC 510
           || ||| | | | || || |   ||||||    |  |   |  || ||||   ||   |
Db     386 GGATTTTCTAACATCGCAACATTCATGGACACTGTGGTGGGCCCTTCTGACAGCAGGCCA 445

Qy     511 GGGAACTGTACTTCGTCCAAGTGGGTTCCCCGGGGCGACTACATCGCCTTCAACACGGAC 570
           |    |||||     ||    ||| | || || ||  |||||||  |  |  ||    ||
Db     446 GACGGCTGTAACAACTCTTCTTGGATCCCTCGTGGAAACTACATAGAATCTAATCGTGAT 505

Qy     571 GAATGCACAGCCACACTGATGTACGCCGTCAACCTGAAGCAATCTGGCACCGTTAACTTC 630
           || ||||| |   |  |||| || || ||  |||| ||| | || |||   ||   |||
Db     506 GACTGCACGGTGTCTTTGATCTATGCTGTGCACCTTAAGAAGTCAGGCTATGTCTTCTTT 565

Qy     631 GAATACTACTATCCAGACTCCAGCATCATCTTTGAGTTTTTCGTTCAGAATGACCAGTGC 690
           || ||| | |||   |||  || |||| |||||||||| ||  |||| ||||| ||||||
Db     566 GAGTACCAGTATGTCGACAACAACATCTTCTTTGAGTTCTTTATTCAAAATGATCAGTGC 625

Qy     691 CAGCCCAATGCAGATGACTC---CAGGTGGATGAAGACCACAGAGAA---AGGATGGGAA 744
           |||   |  |        | |   || |||| | ||    |||.| ||   || |||||
Db     626 CAGGAGATGGACACCACCACTGACAAGTGGGTAAAACTTACAGACAATGGAGAATGGGGC 685

Qy     745 TTCCACAGTGTGGAGCTAAATCGAGGCAATAATGTCCTCTATTGGAGAACCACAGCCTTC 804
           |  ||   |||   ||| ||   ||||| ||  | ||||| |||||||| |||| | ||
Db     686 TCTCATTCTGTAATGCTGAAATCAGGCACAAACATACTCTACTGGAGAACTACAGGCATC 745

Qy     805 TCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTGAGAAACATTGCCATAACAGGGGTG 864
           |  |  | || |    |||||||||||||||| | ||| ||  | ||   |||||||
Db     746 CTTATGGGTTCTAAGGCGGTCAAGCCTGTGCTGGTAAAAAATATCACAATTGAAGGGGTG 805

Qy     865 GCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGCACGTATGCAGACAAGCAGGGCTCC 924
           || ||||| |||||||| || || ||||| || |||||  |       |||| |  || ||
Db     806 GCGTACACATCAGAATGTTTTCCTTGCAAGCCAGGCACATTCAGCAACAAACCAGGTTCA 865

Qy     925 TCTTTCTGCAAACTTTGCCCAGCCAACTCTTATTCAAATAAAGGAGAAACTTCTTGCCAC 984
           |    |||| |  | || ||    ||| | |||||  | |||||||  |     ||
Db     866 TTCAACTGCCAGGTGTGTCCCAGAAACACCTATTCTGAGAAAGGAGCCAAAGAATGTATA 925

Qy     985 CAGTGTGACCCTGACA---AATACTCAGAGAAAGGATCTTCTTCCTGTAACGTGCGCCCA 1041
             |||| |    |||    |||  |||||| |||||||    |   ||||  | ||||||
Db     926 AGGTGTAAAGACGACTCTCAATTTTCAGAGGAAGGATCCAGTGAGTGTACAGAGCGCCCT 985

Qy    1042 GCTTGCACAGACAAAGATTATTTCTACACACACACGGCCTGCGATGCCAACGGAGAGACA 1101
            | || ||    ||||| |||||| | |  || ||  | || ||||   | ||| |||||
Db     986 CCCTGTACCACAAAAGACTATTTCCAGATCCATACTCCATGTGATGAAGAAGGAAAGACA 1045

Qy    1102 CAACTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGCGAGGACCTTGAGGGGGCAGTG 1161
           ||  | |||||||| |||    |||| ||||||||  | |||||  ||    |  ||  |
Db    1046 CAGATAATGTACAAGTGGATAGAGCCCAAAATCTGCCGGGAGGATCTCACAGATGCTATT 1105

Qy    1162 AAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCCTGCAACCCAGGCTTCTTCAAA 1221
           |   ||||  | ||||| | |||||   | || || || ||||||||  || ||  |  ||
Db    1106 AGATTGCCCCCTTCTGGAGAGAAGAAGGATTGTCCGCCTTGCAACCCTGGATTTTATAAC 1165

Qy    1222 ACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCCTACTCCAATGG---CTCAGAC 1278
           |              | ||||| ||||| ||   |||  | |  ||  ||||   |  |||
Db    1166 AATGGATCATCTTCTTGCCATCCCTGTCCTCCTGGAACATTTTCAGATGGAACCAAAGAA 1225

Qy    1279 TGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTTGAATACAAATGGTGGAAC 1338
           ||||  |  || || ||||| || || |||||  | || ||||||||  ||||||||||
Db    1226 TGTAGACCATGTCCAGCAGGAACGGAGCCTGCACTTGGCTTTGAATATAAATGGTGGAAT 1285

Qy    1339 ACGCTGCCCACAAACATGGAAACGACCGTTCTCAGTGGGATCAACTTCGAGTACAAGGGC 1398
           || ||    |||||| |||  ||    ||| ||      || |   ||| | | ||
Db    1286 GTCCTTCCTGGCAACATGAAAACTTCCTGCTTCAATGTTGGGAATTCAAAGTGCGATGGA 1345

Qy    1399 ATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCTGCTGGAGCCTCAGACAAT 1458
           ||||  || ||||||||||||||| ||||| ||  | |  |  |||||||  || ||||||
Db    1346 ATGAATGGTTGGGAGGTGGCTGGAGATCATATCCAGAGTGGGGCTGGAGGTTCTGACAAT 1405

Qy    1459 GACTTCATGATTCTCACTCTGGTTGTGCCAGGATTTAGACCTCCGCAGTCGGTGATGGCA 1518
           || | | ||||  | |   ||  | | |||||||||| ||| ||     ||  ||| | |
Db    1406 GATTACCTGATCTTAAACTTGCATATCCCAGGATTTAAACCACCAACATCTATGACTGGA 1465

Qy    1519 GACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTTGAGACCCTCTGTTCTGTG 1578
           | |||   |  |   ||  | |  ||||| ||||||||||||||||||||||||||| |
Db    1466 GCCAC---GGGTTCTGAACTAGGAAGAATAACATTTGTCTTTGAGACCCTCTGTTCAGCT 1522

Qy    1579 AACTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACCAACACTCCTGTGGAGACG 1638
           ||||||   | |||||||||||||| | | |||   |  |  |  | |  || ||  ||
Db    1523 GACTGTGTTTTGTACTTCATGGTGGATATTAATAGAAAAAGTACAAATGTGGTAGAATCG 1582

Qy    1639 TGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATTGAGGAGAACACTACCACG 1698
           |||   ||  |||||  |||||  | || ||| | |||||     ||||  | ||
Db    1583 TGGGGTGGAACCAAAGAAAAACAAGCTTACACCCATATCATCTTCAAGAATGCAACTTTT 1642

Qy    1699 AGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCAAG 1742
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Db    1643 ACATTTACATGGGGCATTCCCAGAGAACTAATTCAGGGTCCAAG 1686
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Search completed: March 11, 2003, 09:48:41
Job time : 169 secs